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Conference Abstract

Taming the Wild West of Molecular Tools Application in Aquatic Research and Biomonitoring

Alexander M. Weigand[‡], Agnès Bouchez[§], Pieter Boets[|], Kat Bruce[¶], Fedor Ciampor[#], Torbjørn Ekrem[¤], Diego Fontaneto[«], Alain Franc[»], Daniel Hering[^], Maria Kahlert[˅], Emre Keskin[¦], Patricia Mergen[ʔ,ʕ], Jan Pawlowski[¢], Sarah Kueckmann[^], Florian Leese[^]

‡ Musée National d'Histoire Naturelle, Luxembourg, Luxembourg
§ INRA, Thonon, France
| Provincial Centre of Environmental Research, Ghent, Belgium
¶ Nature Metrics Ltd, Egham, United Kingdom
# Slovak Academy of Sciences, Bratislava, Slovakia
¤ NTNU University Museum, Trondheim, Norway
« Institute of Ecosystem Study, Verbania Pallanza, Italy
» BIOGECO, INRA, Université Bordeaux, Cestas, France
^ University of Duisburg-Essen, Essen, Germany
˅ Swedish University of Agricultural Sciences, Uppsala, Sweden
¦ Evolutionary Genetics Laboratory (eGL), Ankara University, Ankara, Turkey
ʔ Meise Botanic Garden, Meise, Belgium
ʕ Royal Museum for Central Africa, Tervuren, Belgium
¢ University of Geneva, Geneve, Switzerland

Corresponding author: Alexander M. Weigand (alexander.weigand@mnhn.lu)

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Abstract

Modern high-throughput sequencing technologies are becoming a game changer in many fields of aquatic research and biomonitoring. To unfold their full potential, however, the independent development of approaches has to be streamlined. This discussion must be fuelled by stakeholders and practitioners and, scientific results collaboratively filtered to identify the most promising avenues. Furthermore, aspects such as time, budget, skills and the application context have to be considered, finally communicating good practice strategies to target audiences.

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Since 2016, the EU COST Action DNAqua-Net is taming the wild west of molecular tools application in aquatic research and biomonitoring. After nucleating available knowledge by the formation of a highly international and transdisciplinary network of scientists, stakeholders, practitioners and enterprises, fields of high methodological diversity were identified. Relevant aspects are currently ground truthed, thereby reducing the plethora of pipelines, parameters and protocols to a subset of good practices or standardisations. To effectively bridge the science-application interface, the very same network is exploited for the dissemination of results (Leese et al. 2018).

The internal working group structure of DNAqua-Net is used to provide an overview of existing methodological fields of diversity in DNA-based aquatic biomonitoring:

WG1 - DNA Barcode References: Different marker systems are targeted for the same organism group. Even in case the same molecular marker is investigated, different primer pairs are frequently applied for DNA metabarcoding. Both aspects challenge the further development of high-quality and complete DNA barcode reference libraries (Weigand et al. 2019).

WG2 - Biotic Indices & Metrics: Index systems are developed from molecular data in various ways: from the estimation of species' biomass (as a proxy for abundance) from sequence reads, to the correlation of presence/absence data of molecular operational taxonomic units (MOTUs) with environmental parameters (Pawlowski et al. 2018).

WG3 - Field & Lab Protocols: Using environmental DNA (eDNA) metabarcoding as an example, diverse sampling techniques based on varying water volumes, different filter systems and collection devices as well as a multitude of laboratory protocols for PCR, replication and sequencing are considered.

WG4 - Data Analysis & Storage: During the process of MOTU identification, varying threshold values and conceptually different pipelines are used, potentially impacting the final list of MOTUs or species retrieved. Furthermore, routine storage concepts for big biodiversity data are only in development and some sample types (e.g. eDNA) have no sophisticated metadata descriptions.

WG5 - Implementation Strategy & Legal Issues: The working group picks up collaboratively filtered good practice strategies and generates room for discussions at the science-policy interface (Hering et al. 2018). The CEN working group WG28 "DNA methods" has been initiated and the development of standardisations is fostered.

Keywords

methods standardisation, DNA-based aquatic biomonitoring, EU COST Action CA15219, Marine Stategy Framework Directive, Water Framework Directive

Presenting author

Alexander M. Weigand

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